

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Arthur A. Branstrom
Donata R. Sizemore
Jerald C. Sadoff
- (ii) TITLE OF INVENTION: Bacterial Delivery System
- 10 (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: John Moran
(B) STREET: USA MRMC - MCMR-JA
(C) CITY: FORT DETRICK, FREDERICK
(D) STATE: MARYLAND
(E) COUNTRY: USA
(F) ZIP: 21702-5012
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0
25 (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
30 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Moran, John
(B) REGISTRATION NUMBER: 26,313
(C) REFERENCE/DOCKET NUMBER:
- 40 (ix) TELECOMMUNICATION INFORMATION
(A) TELEPHONE: (301) 619-2065
(B) TELEFAX: (301) 619-7714
- (2) INFORMATION FOR SEQ ID NO:1:
- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1674 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1

	TCCATAATCA GGATCAATAA AACTGCTGCA GAAATGATTT	40
	CATTCATAAC TCAAATTCCC TGATAATTGC CGCGGACTTT	80
5	CTGCGTGCTA ACAAAGCAGG ATAAGTCGCA TTA CTCATGG	120
	CTTCGCTATC ATTGATTAAT TTCACTTGCG ACTTTGGCTG	160
	CTTTTTGTAT GGTGAAAGAT GTGCCAAGAG GAGACCGGCA	200
	CATTTATACA GCACACATCT TTGCAGGAAA AAAACGCTTA	240
	TGAAAAATGT TGGTTTTATC GGCTGGCGCG GTATGGTCGG	280
10	CTCCGTTCTC ATGCAACGCA TGGTTGAAGA GCGCGACTTC	320
	GACGCCATTC GCCCTGTCTT CTTTTCTACT TCTCAGCTTG	360
	GCCAGGCTGC GCCGTCTTTT GGCGGAACCA CTGGCACACT	400
	TCAGGATGCC TTTGATCTGG AGGCGCTAAA GGCCCTCGAT	440
	ATCATTGTGA CCTGTCAGGG CGGCGATTAT ACCAACGAAA	480
15	TCTATCCAAA GCTTCGTGAA AGCGGATGGC AAGGTTACTG	520
	GATTGACGCA GCATCGTCTC TGCGCATGAA AGATGACGCC	560
	ATCATCATTC TTGACCCCGT CAATCAGGAC GTCATTACCG	600
	ACGGATTAAA TAATGGCATC AGGACTTTTG TTGGCGGTAA	640
	CTGTACCGTA AGCCTGATGT TGATGTCGTT GGGTGGTTTA	680
20	TTCGCCAATG ATCTTGTTGA TTGGGTGTCC GTTGCAACCT	720
	ACCAGGCCGC TTCCGGCGGT GGTGCGCGAC ATATGCGTGA	760
	GTTATTAACC CAGATGGGCC ATCTGTATGG CCATGTGGCA	800
	GATGAACTCG CGACCCCGTC CTCTGCTATT CTCGATATCG	840
	AACGCAAAGT CACAACCTTA ACCCGTAGCG GTGAGCTGCC	880
25	GGTGGATAAC TTTGGCGTGC CGCTGGCGGG TAGCCTGATT	920
	CCGTGGATCG ACAAACAGCT CGATAACGGT CAGAGCCGCG	960
	AAGAGTGGAA AGGGCAGGCG GAAACCAACA AGATCCTCAA	1000

	CACATCTTCC GTAATTCCGG TAGATGGTTT ATGTGTGCGT	1040
	GTCGGGGCAT TGCCTGCCA CAGCCAGGCA TTCACTATTA	1080
	AATTGAAAAA AGATGTGTCT ATTCCGACCG TGGAAGAACT	1120
	GCTGGCTGCG CACAATCCGT GGGCGAAAGT CGTTCCGAAC	1160
5	GATCGGGAAA TCACTATGCG TGAGCTAACC CCAGCTGCCG	1200
	TTACCGGCAC GCTGACCACG CCGGTAGGCC GCCTGCGTAA	1240
	GCTGAATATG GGACCAGAGT TCCTGTCAGC CTTTACCGTG	1280
	GGCGACCAGC TGCTGTGGGG GGCCGCGGAG CCGCTGCGTC	1320
	GGATGCTTCG TCAACTGGCG TAATCTTTAT TCATTAAATC	1360
10	TGGGGCGCGA TGCCGCCCCT GTTAGTGCGT AATACAGGAG	1400
	TAAGCGCAGA TGTTCATGA TTTACCGGGA GTTAAATAGA	1440
	GCATTGGCTA TTCTTTAAGG GTGGCTGAAT ACATGAGTAT	1480
	TCACAGCCTT ACCTGAAGTG AGGACGACGC AGAGAGGATG	1520
	CACAGAGTGC TGCGCCGTTT AGGTCAAAAA AATGTCACAA	1560
15	CCAGAAGTCA AAAATCCAAT TGGATGGGGT GACACAATAA	1600
	AACAGGAAGA CAAGCATGTC CGATCGTATC GATAGAGACG	1640
	TGATTAACGC GCTAATTGCA GGCCATTTTG CGGA	1674

(3) INFORMATION FOR SEQ ID NO:2:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1121 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Other nucleic acid
- (A) DESCRIPTION: The *E. coli asd* gene coding for β -aspartic semialdehyde dehydrogenase identified in SEQ ID NO:1 was modified by deleting 553 bp from position 439 to 991.
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

TCCATAATCA GGATCAATAA AACTGCTGCA GAAATGATTT	40
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	CATTCATAAC TCAAATTCCC TGATAATTGC CGCGGACTTT	80
	CTGCGTGCTA ACAAAGCAGG ATAAGTCGCA TTAATCATGG	120
	CTTCGCTATC ATTGATTAAT TTCACCTGCG ACTTTGGCTG	160
	CTTTTTGTAT GGTGAAAGAT GTGCCAAGAG GAGACCGGCA	200
5	CATTTATACA GCACACATCT TTGCAGGAAA AAAACGCTTA	240
	TGAAAAATGT TGGTTTTATC GGCTGGCGCG GTATGGTCGG	280
	CTCCGTTCTC ATGCAACGCA TGGTTGAAGA GCGCGACTTC	320
	GACGCCATTC GCCCTGTCTT CTTTTCTACT TCTCAGCTTG	360
	GCCAGGCTGC GCCGTCTTTT GGCGGAACCA CTGGCACACT	400
10	TCAGGATGCC TTTGATCTGG AGGCGCTAAA GGCCCTCGGA	440
	TCCTCAACAC ATCTTCCGTA ATTCCGGTAG ATGGTTTATG	480
	TGTGCGTGTC GGGGCATTGC GCTGCCACAG CCAGGCATTC	520
	ACTATTAAAT TGAAAAAAGA TGTGTCTATT CCGACCGTGG	560
	AAGAACTGCT GGCTGCGCAC AATCCGTGGG CGAAAGTCGT	600
15	TCCGAACGAT CGGGAAATCA CTATGCGTGA GCTAACCCCA	640
	GCTGCCGTTA CCGGCACGCT GACCACGCCG GTAGGCCGCC	680
	TGCGTAAGCT GAATATGGGA CCAGAGTTCC TGTCAGCCTT	720
	TACCGTGGGC GACCAGCTGC TGTGGGGGGC CGCGGAGCCG	760
	CTGCGTCGGA TGCTTCGTCA ACTGGCGTAA TCTTTATTCA	800
20	TTAAATCTGG GGCGCGATGC CGCCCCTGTT AGTGCGTAAT	840
	ACAGGAGTAA GCGCAGATGT TTCATGATTT ACCGGGAGTT	880
	AAATAGAGCA TTGGCTATTC TTTAAGGGTG GCTGAATACA	920
	TGAGTATTCA CAGCCTTACC TGAAGTGAGG ACGACGCAGA	960
	GAGGATGCAC AGAGTGCTGC GCCGTTTCAGG TCAAAAAAAT	1000
25	GTCACAACCA GAAGTCAAAA ATCCAATTGG ATGGGGTGAC	1040
	ACAATAAAAC AGGAAGACAA GCATGTCCGA TCGTATCGAT	1080
	AGAGACGTGA TTAACGCGCT AATTGCAGGC CATTTTGCGG	1120

(4) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3
AGATCTCCCT GATAATTGCC GC

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(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 26 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

AGATCTCGCT TACTCCTGTA TTACGC

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30 (6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

CGAGGGCCTT TAGCGCCTCC

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(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GATCCTCAAC ACATCTTCCG

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5 (8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic acid

10 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

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GAGCTCCCCT GATAATTGCC GC

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(9) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

30 GTCGACCGCT TACTCCTGTA TTACGC

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